Biosynthesis of IAA in *Pseudomonas savastanoi*: a comparative genomic approach.

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Bacteria belonging to the *Pseudomonas syringae* complex cause diseases in a variety of woody and herbaceous plants. *Pseudomonas savastanoi* is a member of this complex and produces tumors or excrescences in the aerial parts of woody plants. The species is classified into four pathovars, i.e. savastanoi (Psv, olive), nerii (Psn, oleander), retacarpa (Psr, Spanish broom) and fraxini (Psf, ash). Our research group have carried out the sequencing, annotation and comparative analysis of the genomes of several strains belonging to these pathovars. These analyses have identified the set of genes belonging to the *P. savastanoi* pan-genome and the collection of pathovar- and strain-specific genes. Through the web app PIFAR (Plant-bacterium Interaction Factors Resource) we have determined the presence of potential virulence factors involved in the interaction of these pathovars with their hosts. Special attention was given to genes putatively involved in the production of indole-3-acetic acid (IAA), a pathogenicity factor in these bacteria. With the exception of Psf, *P. savastanoi* strains produce IAA from tryptophan through the indole-3-acetamide pathway (*iaaM* and *iaaH* genes). We have shown that a Psv *ΔiaaMH* mutant drastically reduces IAA levels. However, this mutant produces amounts of this phytohormone similar to those synthesized by Psf strains. We are currently analyzing the role of several Psv genes in the biosynthesis of IAA through alternative pathways.